





PROSITE: PS00179: AA: tRNA-LIGASE [1, 12, 13]  
 KW: AIP binding: Aminoacyl-tRNA synthetase: Ligase: Protein-protein  
 SEQUENCE: 464 AA: 52619 MW: 2703514140.0904 kDa

Query Match 48.98: Score 42.52: ID: 4: Length 4: 4  
 Best Local Similarity: 62.58: Pred. No. 45:  
 Matches: 10: Conservative: 4: Mismatches: 2: Gaps: 1:

4 EELKFAAHYNEIL 17  
 111 111 111 111  
 20 ESTIRFAAHNEIL 218

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161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614
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108 1081 : 2 44802 ; 0AAB4 449 . 1 ; 001NEB3  
108 1081 : 2 44802 ; 0AAB4 449 . 1 ;  
108 1081 : 2 44802 ; 0AAB4 449 . 1 ; 001NEB3  
108 1081 : 2 44802 ; 0AAB4 449 . 1 ; 001NEB3

161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614
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[illegible]

Survey Month	48, 48	Score 42,	198 57	Length 100 2
First Food Similarity	54, 58	Prod. No. 4,	198 57	
Marches	6	Survey with 100	4	Mismatches 1

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[illegible]

	Quality	47-100	Score 47-100	Level 1-5000
	Post Local Similarity	50-100	Fold No. 1-2	
	Matrixes	7: Conservative	4: Mismatches	0-100%
-3-	4 FETTERBAHNIE 15			
	11 11 11 11 11			
16	21 DELTAFAVORINSK 44			

RESULT 13		
ID	PRELIMINARY	PRJ
000004		2 x 8 AA.
01	01 NOV-1999 (TREMbled, 12, treated)	
01	01 NOV-1999 (TREMbled, 12, last segment update)	
01	01 JAN-2001 (TREMbled, 12, last segment update)	
02	HYPOBETICAL 26.0 KDA PROTEIN ADP0R24.	
03	ADP0R24.	

OS Acetylcytochrome P-450: A cytochrome P-450 subfamily I enzyme from *Acetivibrio* sp.  
OX Nal.oxid. 566-66;  
KN 11  
SEQUENCE FROM N.A.  
KO SIKAMIN KL  
RX METAL-BINDING SITE, PROBABLY IRON-BINDING  
KA KIMURA, Y., YAMAMOTO, Y., HIRANO, Y., HOSHINO, H., YAMAZAKI, S., HASEGAWA, Y.  
KA KIMURA, Y., HIRANO, Y., YAMAMOTO, Y., HOSHINO, H., YAMAZAKI, S., HASEGAWA, Y.  
KA HASEGAWA, Y., KIMURA, Y., HIRANO, Y., YAMAMOTO, Y., HOSHINO, H., YAMAZAKI, S.,  
KA TAKAHASHI, M., MURAKAMI, S., FUJIMOTO, T., TAKAKURA, K., KIMURA, Y.,  
KA YAMAZAKI, S., KIMURA, Y., HIRANO, Y., YAMAMOTO, Y., HOSHINO, H., YAMAZAKI, S.,  
KA KIMURA, Y., YAMAMOTO, Y., HIRANO, Y., YAMAMOTO, Y., HOSHINO, H., YAMAZAKI, S.,  
KA "Complete genome sequence of an aerobic hyper-thermophilic  
KA *Thermotoga* sp. Acetivibrio form. KL 11  
KA (66 Res. 6, 65-66) (1999)  
LO EMIL: AP000000: BAA70804.1;  
LO INTERLOC: PROPOD01: 20; MIPROD01:  
LO PROSITE: PS00124: 2176; PROSITE: PS00124: 2176;  
KO Hyperthermophilic protein: complete genome  
NO SEQUENCE: 2,45 AA: 2,594 AA: 2,690 AA: 2,795 AA: 2,894 AA: 2,994 AA: 3,094 AA: 3,194 AA: 3,294 AA: 3,394 AA: 3,494 AA: 3,594 AA: 3,694 AA: 3,794 AA: 3,894 AA: 3,994 AA: 4,094 AA: 4,194 AA: 4,294 AA: 4,394 AA: 4,494 AA: 4,594 AA: 4,694 AA: 4,794 AA: 4,894 AA: 4,994 AA: 5,094 AA: 5,194 AA: 5,294 AA: 5,394 AA: 5,494 AA: 5,594 AA: 5,694 AA: 5,794 AA: 5,894 AA: 5,994 AA: 6,094 AA: 6,194 AA: 6,294 AA: 6,394 AA: 6,494 AA: 6,594 AA: 6,694 AA: 6,794 AA: 6,894 AA: 6,994 AA: 7,094 AA: 7,194 AA: 7,294 AA: 7,394 AA: 7,494 AA: 7,594 AA: 7,694 AA: 7,794 AA: 7,894 AA: 7,994 AA: 8,094 AA: 8,194 AA: 8,294 AA: 8,394 AA: 8,494 AA: 8,594 AA: 8,694 AA: 8,794 AA: 8,894 AA: 8,994 AA: 9,094 AA: 9,194 AA: 9,294 AA: 9,394 AA: 9,494 AA: 9,594 AA: 9,694 AA: 9,794 AA: 9,894 AA: 9,994 AA: 10,094 AA: 10,194 AA: 10,294 AA: 10,394 AA: 10,494 AA: 10,594 AA: 10,694 AA: 10,794 AA: 10,894 AA: 10,994 AA: 11,094 AA: 11,194 AA: 11,294 AA: 11,394 AA: 11,494 AA: 11,594 AA: 11,694 AA: 11,794 AA: 11,894 AA: 11,994 AA: 12,094 AA: 12,194 AA: 12,294 AA: 12,394 AA: 12,494 AA: 12,594 AA: 12,694 AA: 12,794 AA: 12,894 AA: 12,994 AA: 13,094 AA: 13,194 AA: 13,294 AA: 13,394 AA: 13,494 AA: 13,594 AA: 13,694 AA: 13,794 AA: 13,894 AA: 13,994 AA: 14,094 AA: 14,194 AA: 14,294 AA: 14,394 AA: 14,494 AA: 14,594 AA: 14,694 AA: 14,794 AA: 14,894 AA: 14,994 AA: 15,094 AA: 15,194 AA: 15,294 AA: 15,394 AA: 15,494 AA: 15,594 AA: 15,694 AA: 15,794 AA: 15,894 AA: 15,994 AA: 16,094 AA: 16,194 AA: 16,294 AA: 16,394 AA: 16,494 AA: 16,594 AA: 16,694 AA: 16,794 AA: 16,894 AA: 16,994 AA: 17,094 AA: 17,194 AA: 17,294 AA: 17,394 AA: 17,494 AA: 17,594 AA: 17,694 AA: 17,794 AA: 17,894 AA: 17,994 AA: 18,094 AA: 18,194 AA: 18,294 AA: 18,394 AA: 18,494 AA: 18,594 AA: 18,694 AA: 18,794 AA: 18,894 AA: 18,994 AA: 19,094 AA: 19,194 AA: 19,294 AA: 19,394 AA: 19,494 AA: 19,594 AA: 19,694 AA: 19,794 AA: 19,894 AA: 19,994 AA: 20,094 AA: 20,194 AA: 20,294 AA: 20,394 AA: 20,494 AA: 20,594 AA: 20,694 AA: 20,794 AA: 20,894 AA: 20,994 AA: 21,094 AA: 21,194 AA: 21,294 AA: 21,394 AA: 21,494 AA: 21,594 AA: 21,694 AA: 21,794 AA: 21,894 AA: 21,994 AA: 22,094 AA: 22,194 AA: 22,294 AA: 22,394 AA: 22,494 AA: 22,594 AA: 22,694 AA: 22,794 AA: 22,894 AA: 22,994 AA: 23,094 AA: 23,194 AA: 23,294 AA: 23,394 AA: 23,494 AA: 23,594 AA: 23,694 AA: 23,794 AA: 23,894 AA: 23,994 AA: 24,094 AA: 24,194 AA: 24,294 AA: 24,394 AA: 24,494 AA: 24,594 AA: 24,694 AA: 24,794 AA: 24,894 AA: 24,994 AA: 25,094 AA: 25,194 AA: 25,294 AA: 25,394 AA: 25,494 AA: 25,594 AA: 25,694 AA: 25,794 AA: 25,894 AA: 25,994 AA: 26,094 AA: 26,194 AA: 26,294 AA: 26,394 AA: 26,494 AA: 26,594 AA: 26,694 AA: 26,794 AA: 26,894 AA: 26,994 AA: 27,094 AA: 27,194 AA: 27,294 AA: 27,394 AA: 27,494 AA: 27,594 AA: 27,694 AA: 27,794 AA: 27,894 AA: 27,994 AA: 28,094 AA: 28,194 AA: 28,294 AA: 28,394 AA: 28,494 AA: 28,594 AA: 28,694 AA: 28,794 AA: 28,894 AA: 28,994 AA: 29,094 AA: 29,194 AA: 29,294 AA: 29,394 AA: 29,494 AA: 29,594 AA: 29,694 AA: 29,794 AA: 29,894 AA: 29,994 AA: 30,094 AA: 30,194 AA: 30,294 AA: 30,394 AA: 30,494 AA: 30,594 AA: 30,694 AA: 30,794 AA: 30,894 AA: 30,994 AA: 31,094 AA: 31,194 AA: 31,294 AA: 31,394 AA: 31,494 AA: 31,594 AA: 31,694 AA: 31,794 AA: 31,894 AA: 31,994 AA: 32,094 AA: 32,194 AA: 32,294 AA: 32,394 AA: 32,494 AA: 32,594 AA: 32,694 AA: 32,794 AA: 32,894 AA: 32,994 AA: 33,094 AA: 33,194 AA: 33,294 AA: 33,394 AA: 33,494 AA: 33,594 AA: 33,694 AA: 33,794 AA: 33,894 AA: 33,994 AA: 34,094 AA: 34,194 AA: 34,294 AA: 34,394 AA: 34,494 AA: 34,594 AA: 34,694 AA: 34,794 AA: 34,894 AA: 34,994 AA: 35,094 AA: 35,194 AA: 35,294 AA: 35,394 AA: 35,494 AA: 35,594 AA: 35,694 AA: 35,794 AA: 35,894 AA: 35,994 AA: 36,094 AA: 36,194 AA: 36,294 AA: 36,394 AA: 36,494 AA: 36,594 AA: 36,694 AA: 36,794 AA: 36,894 AA: 36,994 AA: 37,094 AA: 37,194 AA: 37,294 AA: 37,394 AA: 37,494 AA: 37,594 AA: 37,694 AA: 37,794 AA: 37,894 AA: 37,994 AA: 38,094 AA: 38,194 AA: 38,294 AA: 38,394 AA: 38,494 AA: 38,594 AA: 38,694 AA: 38,794 AA: 38,894 AA: 38,994 AA: 39,094 AA: 39,194 AA: 39,294 AA: 39,394 AA: 39,494 AA: 39,594 AA: 39,694 AA: 39,794 AA: 39,894 AA: 39,994 AA: 40,094 AA: 40,194 AA: 40,294 AA: 40,394 AA: 40,494 AA: 40,594 AA: 40,694 AA: 40,794 AA: 40,894 AA: 40,994 AA: 41,094 AA: 41,194 AA: 41,294 AA: 41,394 AA: 41,494 AA: 41,594 AA: 41,694 AA: 41,794 AA: 41,894 AA: 41,994 AA: 42,094 AA: 42,194 AA: 42,294 AA: 42,394 AA: 42,494 AA: 42,594 AA: 42,694 AA: 42,794 AA: 42,894 AA: 42,99

Group Match	47-197	Score 41, 48-17	Location 203
Host Local Simulation	2, 997	Prod. No. 407	
Matches	97	Consecutive	77
		Missed	22

QY	2	EHIKFAAHYNIEIK	IR
		I I I I I I I I	
Id	94	HVVIKFIVAHVVAVIK	III

— 14 —

[illegible]

Query Match	47.1%	Score 41	14	11	Length 20
Post-Similarity	61.7%	Insert No.	44		
Matches	82	Conserved	22	Mismatches	4
				Indels	0
				Gaps	0
CY	6	KKAAHYNLELK	18		
	111	111	11		
DB	94	KKAAPYDLELK	105		

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Result: 15
P0704b:
ID: P0704b      DEFINITION: PKC      458 AA
AC: P0704b
PI: 01 MAY 1997 (EMBL) 03 (Genbank)
OI: 01 MAY 1997 (EMBL) 03 (Genbank)
DI: 01 JUN 2001 (EMBL) 17 (Last annotation update)
DE: VASCULAR ENDOTHELIAL GROWTH FACTOR D (V-EGF) INDUCED BY WITH FACTOR
EN: VEGF to be EGFR
OS: Mus musculus (Mouse)
OC: Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC: Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus
OX: NCBI TaxID: 10090
PI: 11
PR: FREQUENTLY FROM N.A.
PC: STRAIN 9706/24; PubMed 9706/24
PX: MEDLINE 9706/24; PubMed 9706/24
PA: Chondrich M. Muroganin L. Fournier R. et al (1997) R.
PI: Identification of a c-fos induced gene that is related to the
PI: placental derived growth factor/vascular endothelial growth factor
PI: family.
PI: Proc. Natl. Acad. Sci. U.S.A. 94:11675-11679(1997).
PI: 121
PR: SEQUENCE FROM N.A.
PC: TISSUE: LUNG
PX: MEDLINE 9706/24; PubMed 9706/24
PA: Yamada Y., Nishii T., Shimizu M., Hirata Y.
PI: "Molecular cloning of a novel vascular endothelial growth factor-
PI: like protein."
PI: VEGF D.
PI: Genomics 4:2483-2486(1997).
PI: EMBL: X99572; CAA67892.1;
PI: EMBL: U09628; AAA14002.1;
PI: HSSRP: P16692; VPP.
PI: MED: 97110607; EMBL:
PI: Tissue: 190000/22; PKC;
PI: Tissue: 190000/11; PKC;
PI: Tissue: 190000/20; PKC;
PI: SMAR1: SM00141; PKC;
PI: PROSITE: PS00249; PKC;
PI: PROSITE: PS00278; PKC;
PI: SEQUENCE FOR AA: 40000 MW: 46.604/1900/0.67 0706/24
2007: Match 47/19; Score 41; DB 11; Length 458;
Foot: Local similarity: 61.5%; Foot: No; 48;
Matches: 8; Overlap: 27; Mismatches: 3; Indels: 0; Gaps: 0;
27: 6. KFAAAYNTEIK 18
ID: 6. KFAAAYNTEIK 105

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Search completed: February 22, 2002, 15:47:58  
 Database: 116, 500

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[illegible]

February 22, 2002, 15:36:27 : Submitted from a web browser

[illegible]

Scoring table:  $\text{KJ-SIM62}$   
 Group 10.0, Group 0.0

140059 Sols, 46664827 seconds

Local number of hits satisfying chosen parameters: 10000

[illegible]

**Maximum Job Set Length:** 20000000

Post = Process; Min = Minimum; Mat = Material; Cost = Cost; and

Maximum Moisture

Listing first 45 summaries

Mathematics : Swissb1 (1) 1 - 49 : \*

pred. No. is the number of results predicted by chance too high a score greater than or equal to the score of the result being printed and is derived by analyzing the total score distribution.

Result No.	Score	Country	Match	Length	DB	ID	Summary
1	86	USA	98.7	419	1	VERB_HUMAN	147077 human structure
2	73	USA	84.9	415	1	VERB_MACHINE	147078 human structure
3	45.5	USA	52.3	1063	1	DETM_CLAUDE	147079 human structure
4	42	USA	49.3	648	1	PROPR_PERSON	147080 human structure
5	41	USA	47.1	450	1	GRAMM_SENTENCE	147081 human structure
6	41	USA	47.1	843	1	POLA_QUESTION	147082 human structure
7	40	USA	46.0	188	1	SYND_TITLE	147083 human structure
8	39.5	USA	45.4	882	1	YHAB_SCHEMA	147084 human structure
9	39	USA	44.8	329	1	129_ASYNTH	147085 human structure
10	39	USA	44.8	783	1	VERB_PERSON	147086 human structure
11	38.5	USA	44.3	754	1	BUTR_PERSON	147087 human structure
12	38.5	USA	44.3	1095	1	CONF_YEAST	147088 human structure
13	38	USA	43.7	155	1	FOOD_MACHINE	147089 human structure
14	38	USA	43.7	343	1	YD57_MACHINE	147090 human structure
15	38	USA	43.7	447	1	DNAME_SYNTAX	147091 human structure
16	38	USA	43.7	437	1	PROB_MACHINE	147092 human structure
17	38	USA	43.7	651	1	VD47_HSV6G	147093 human structure
18	38	USA	43.7	651	1	VD47_HSV6G	147094 human structure
19	38	USA	43.7	800	1	PT11_YEAST	147095 human structure
20	37	USA	43.7	2113	1	PROB_YEAST	147096 human structure
21	37.5	USA	43.1	154	1	PAU1_MACHINE	147097 human structure
22	37.5	USA	43.1	1197	1	PROB_MACHINE	147098 human structure
23	37	USA	42.5	174	1	KAD_MACHINE	147099 human structure
24	37	USA	42.5	174	1	KAD_MACHINE	147100 human structure
25	37	USA	42.5	174	1	KAD_MACHINE	147101 human structure
26	37	USA	42.5	174	1	KAD_MACHINE	147102 human structure
27	37	USA	42.5	174	1	KAD_MACHINE	147103 human structure
28	37	USA	42.5	215	1	KAD_MACHINE	147104 human structure
29	37	USA	42.5	215	1	KAD_MACHINE	147105 human structure
30	37	USA	42.5	215	1	KAD_MACHINE	147106 human structure
31	37	USA	42.5	310	1	PROB_MACHINE	147107 human structure
32	37	USA	42.5	359	1	PROB_MACHINE	147108 human structure
33	37	USA	42.5	422	1	PROB_MACHINE	147109 human structure

RESULT 1		ALIGNMENTS	
VERB_HUMAN	STANDARD:	VERB_HUMAN	VERB_MOUSE
1	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
2	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
3	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
4	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
5	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
6	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
7	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
8	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
9	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
10	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
11	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
12	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
13	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
14	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
15	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
16	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
17	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
18	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
19	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
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43	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
44	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE
45	VERB_HUMAN	VERB_HUMAN	VERB_MOUSE



Query Match	Score	Length
Best Local Similarity	62.48%	1000
Matched for Consistency	27	Mismatches: 4

	18-48	Stout 42	DB 12	Leath 548
Grain Moisture	50.00	50.00	50.00	50.00
Root Taper Similarity	50.00	50.00	50.00	50.00
Matchups	7	Matchups	4	Matchups
QY	4	ELIKFAAHNHET 16		
DB	243	KIVNIAAHYDOL 256		

RESULT 5			
DRAA SECT			
ID	DNA_SEQ1	STANDARD	PRG 450 AA
A2	p44028		
D1	01-FEB-1994 (rel. 28; (revised))		
D1	01-FEB-1994 (rel. 28; (last sequence update))		
D1	20 AUG 2001 (rel. 40; (last annotation update))		
D2	CHICKEN-306A1, REPLICATION INITIATOR PROTEIN DRAA.		
D3	DRAA.		
D5	SPIROPLASMA C1171.		
D6	Bacterioid, Firmicutes, Bacillus/Clostridium group; Mollicutes;		
D6	SPIROPLASMA20000; Spiroplasma.		
D8	NH1_taxid 21345		
D8	11		
D9	SEQUENCE FROM N.A.		
D9	STRAIN A127 27556 / 88A2.		
D9	CELLINE 94109261; PubMed 7744084		
D9	Yo F., Renaudin J., Kovo J.M., Talipet F.		
D9	"Cloning and sequencing of the replication origin (ori) of the		
D9	Spiroplasma c1171 chromosome and construction of autonomously		
D9	replicating artificial plasmids."		
D9	Cell. Microbiol. 25:23-29(1994).		
D9	12		
D9	SEQUENCE OF 147-411 FROM N.A.		
D9	STRAIN A127 27556 / 88A2.		
D9	CELLINE 94109261; PubMed 8282191		
D9	Yoshida K., Miyake H., Yokumura T.		
D9	"Comparison of the conserved region in the draa gene from three		
D9	molluscic species."		
D9	FEBS Microbiol. Lett. 114:229-24(1994).		
D9	13		
D9	SEQUENCE OF 147-411 FROM N.A.		
D9	STRAIN A127 27556 / 88A2.		
D9	CELLINE 94109261; PubMed 8282191		
D9	Yoshida K., Miyake H., Yokumura T.		
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D9	molluscic species."		
D9	FEBS Microbiol. Lett. 114:229-24(1994).		
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D9	CELLINE 94109261; PubMed 8282191		
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D9	CELLINE 94109261; PubMed 8282191		
D9	Yoshida K., Miyake H., Yokumura T.		
D9	"Comparison of the conserved region in the draa gene from three		
D9	molluscic species."		
D9	FEBS Microbiol. Lett. 114:229-24(1994).		
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D9	SEQUENCE OF 147-411 FROM N.A.		
D9	STRAIN A127 27556 / 88A2.		
D9	CELLINE 94109261; PubMed 8282191		
D9	Yoshida K., Miyake H., Yokumura T.		
D9	"Comparison of the conserved region in the draa gene from three		
D9	molluscic species."		
D9	FEBS Microbiol. Lett. 114:229-24(1994).		
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D9	SEQUENCE OF 147-411 FROM N.A.		
D9	STRAIN A127 27556 / 88A2.		
D9	CELLINE 94109261; PubMed 8282191		
D9	Yoshida K., Miyake H., Yokumura T.		
D9	"Comparison of the conserved region in the draa gene from three		
D9	molluscic species."		
D9	FEBS Microbiol. Lett. 114:229-24(1994).		
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D9	SEQUENCE OF 147-411 FROM N.A.		
D9	STRAIN A127 27556 / 88A2.		
D9	CELLINE 94109261; PubMed 8282191		
D9	Yoshida K., Miyake H., Yokumura T.		
D9	"Comparison of the conserved region in the draa gene from three		
D9	molluscic species."		
D9	FEBS Microbiol. Lett. 114:229-24(1994).		
D9	21		

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[illegible]







[illegible]





[illegible]















[illegible][illegible]





```

1 ADDRESS: STEIN, KENNETH, COLUMBIEN & FOX
2 STREET: 1100 NEW YORK AVENUE
3 CITY: WASHINGTON
4 STATE: DC
5 COUNTRY: USA
6 ZIP: 20002
7 CURRENT APPOINTMENT FORM:
8 MEDIUM TYPE: floppy disk
9 OPERATING SYSTEM: DOS/MS-DOS
10 SOFTWARE: Patented in Romania #1.0, Version #1.0
11 CURRENT APPOINTMENT DATA:
12 APPOINTMENT NUMBER: 05/07/2001.105
13 FILING DATE: 05/07/2001
14 CLASSIFICATION:
15 PREVIOUS APPOINTMENT DATA:
16 APPOINTMENT NUMBER: 05/05/2001.100
17 FILING DATE: 05 MAR 1994
18 CLASSIFICATION:
19 PREVIOUS APPOINTMENT DATA:
20 APPOINTMENT NUMBER: 05/05/2001.100
21 FILING DATE: 24 JAN 1997
22 CLASSIFICATION:
23 ALTERNATIVE NAME: STEIN, KENNETH
24 IDENTIFICATION NUMBER: 05,000
25 REFERENCE: 05,001,000000, 1000, 10,000,000
26 IDENTIFICATION INFORMATION:
27 TELEPHONE: (202) 771,2640
28 TELEFAX: (202) 771,2640
29 INFORMATION FOR STEIN, KENNETH:
30 CURRENT CHARACTERISTICS:
31 LENGTH: 419 amino acids
32 TYPE: amino acid
33 SIGNIFICANCE:
34 POLARITY: linear
35 MOLECULAR TYPE: protein
36 US OR 705,430,000
37
38 GENE: MATCH 08,000,000, 100,000, 100,000, 100,000, 100,000
39 BEST LOCAL SIMILARITY: 100,000, 100,000, 100,000, 100,000, 100,000
40 MATCHES: 17, 100,000, 100,000, 100,000, 100,000, 100,000
41
42 2. IDENTIFICATION NUMBER: 10
43 ID: 101 IDENTIFICATION NUMBER: 100
44
45 RESULT: 14
46 US OR 705,430,000
47 SOFTWARE: Patented in Romania #1.0, Version #1.0
48 CURRENT APPOINTMENT DATA:
49 APPOINTMENT NUMBER: 05/07/2001.105
50 FILING DATE:
51 PREVIOUS APPOINTMENT DATA:
52 APPOINTMENT NUMBER: 05/07/2001.105
53 FILING DATE: 05/07/2001
54 CLASSIFICATION:
55 PREVIOUS APPOINTMENT DATA:
56 APPOINTMENT NUMBER: 05/07/2001.105
57 FILING DATE: 05 MAR 1994
58 CLASSIFICATION:
59 PREVIOUS APPOINTMENT DATA:
60 APPOINTMENT NUMBER: 05/07/2001.105
61 FILING DATE: 24 JAN 1997
62 CLASSIFICATION:
63 ALTERNATIVE NAME: STEIN, KENNETH
64 IDENTIFICATION NUMBER: 05,000
65 REFERENCE: 05,001,000000, 1000, 10,000,000
66 IDENTIFICATION INFORMATION:
67 TELEPHONE: (202) 771,2640
68 TELEFAX: (202) 771,2640
69 INFORMATION FOR STEIN, KENNETH:
70 CURRENT CHARACTERISTICS:
71 LENGTH: 419 amino acids
72 TYPE: amino acid
73 SIGNIFICANCE:
74 POLARITY: linear
75 MOLECULAR TYPE: protein
76 US OR 705,430,000

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1 SOFTWARE: Patented in Romania #1.0, Version #1.0
2 CURRENT APPOINTMENT DATA:
3 APPOINTMENT NUMBER: 05/07/2001.105
4 FILING DATE:
5 PREVIOUS APPOINTMENT DATA:
6 APPOINTMENT NUMBER: 05/07/2001.105
7 FILING DATE: 05/07/2001
8 CLASSIFICATION:
9 PREVIOUS APPOINTMENT DATA:
10 APPOINTMENT NUMBER: 05/07/2001.105
11 FILING DATE: 05 MAR 1994
12 CLASSIFICATION:
13 PREVIOUS APPOINTMENT DATA:
14 APPOINTMENT NUMBER: 05/07/2001.105
15 FILING DATE: 24 JAN 1997
16 CLASSIFICATION:
17 ALTERNATIVE NAME: STEIN, KENNETH
18 IDENTIFICATION NUMBER: 05,000
19 REFERENCE: 05,001,000000, 1000, 10,000,000
20 IDENTIFICATION INFORMATION:
21 TELEPHONE: (202) 771,2640
22 TELEFAX: (202) 771,2640
23 INFORMATION FOR STEIN, KENNETH:
24 CURRENT CHARACTERISTICS:
25 LENGTH: 419 amino acids
26 TYPE: amino acid
27 SIGNIFICANCE:
28 POLARITY: linear
29 MOLECULAR TYPE: protein
30 US OR 705,430,000
31
32 GENE: MATCH 08,000,000, 100,000, 100,000, 100,000, 100,000
33 BEST LOCAL SIMILARITY: 100,000, 100,000, 100,000, 100,000, 100,000
34 MATCHES: 17, 100,000, 100,000, 100,000, 100,000, 100,000
35
36 2. IDENTIFICATION NUMBER: 10
37 ID: 101 IDENTIFICATION NUMBER: 100
38
39 RESULT: 14
40 US OR 705,430,000
41 SOFTWARE: Patented in Romania #1.0, Version #1.0
42 CURRENT APPOINTMENT DATA:
43 APPOINTMENT NUMBER: 05/07/2001.105
44 FILING DATE:
45 PREVIOUS APPOINTMENT DATA:
46 APPOINTMENT NUMBER: 05/07/2001.105
47 FILING DATE: 05/07/2001
48 CLASSIFICATION:
49 PREVIOUS APPOINTMENT DATA:
50 APPOINTMENT NUMBER: 05/07/2001.105
51 FILING DATE: 05 MAR 1994
52 CLASSIFICATION:
53 PREVIOUS APPOINTMENT DATA:
54 APPOINTMENT NUMBER: 05/07/2001.105
55 FILING DATE: 24 JAN 1997
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59 REFERENCE: 05,001,000000, 1000, 10,000,000
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63 INFORMATION FOR STEIN, KENNETH:
64 CURRENT CHARACTERISTICS:
65 LENGTH: 419 amino acids
66 TYPE: amino acid
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68 POLARITY: linear
69 MOLECULAR TYPE: protein
70 US OR 705,430,000

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 13 Altitude Sickness  
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 14 WtG 1999 10/15/99/40  
 16 N 15000 AAZ100 2.8  
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 18 New human vascular endothelial growth factor polypeptide 2  
 19 used to develop products for treating, e.g., cancers, or damage to  
 20 wounds, and angiogenesis or for wound healing or tissue  
 21 remodeling  
 22 Claim 1, Page 11, 11%, 17pp; finalish  
 23  
 24 The vascular endothelial growth factor 2 (VEGF-2) polypeptides have  
 25 activities affecting growth and migration of vascular endothelial cells,  
 26 promoting growth of lymphatic endothelial cells and lymphatic vessels,  
 27 increasing vascular permeability, and affecting myelopoiesis. The  
 28 products can be used for stimulating angiogenesis, for inhibiting  
 29 angiogenesis, for stimulating lymphatopoiesis, treatment or prevention  
 30 of inflammation, edema, rheumatoid arthritis, or Multiple Sclerosis. They can  
 31 also be used to modulate myelopoiesis, e.g., treatment of anemia.  
 32 They can also be used for modulating the growth of endothelial cells,  
 33 or to promote or inhibit trafficking of leukocytes between tissues and  
 34 lymphatic vessels or to affect migration in and out of the thymus.  
 35 Sequence: 419 AA;  
 36  
 37 Query Match 98.98% Score 862 106 119 Length 419  
 38 best local similarity 100.00% Prod. No. 4360 0/2  
 39 Method: 1/2: consensus 0/2 Mismatches 0/2 Indels 0/2 Gaps 0/2  
 40  
 41 2 EELIKFAAHYNTEIK 16  
 42 104 001K1KaaHygn01K 120  
 43  
 44 EELIKFAAHYNTEIK 16  
 45 AAY00510  
 46 AAY00510 standard: Protein: 419 AA  
 47  
 48 AAY00510  
 49 16 Nov 1999 (first entry)  
 50  
 51 Vascular endothelial growth factor 2 (Vegf 2).  
 52  
 53 Human vascular endothelial growth factor 2: VEGF-2  
 54 vascular endothelial cell growth endothelial cell mitogenic  
 55 endothelial cell growth promoting blood flow; immune system  
 56 immune cell; cancer; autoimmune disorder; blood pressure; edema;  
 57 edema; inflammation; common variable immunodeficiency;  
 58 leukocyte adhesion deficiency syndrome; HIV; HIV infection;  
 59 phagocyte; leukocyte; dysfunction; severe combined immunodeficiency;  
 60 Wiskott Aldrich disorder; anemia; thrombocytopoiesis; hemofilirosis;  
 61 allergy; asthma; allergic asthma;  
 62  
 63 human; asthma;  
 64  
 65 W090504 A1  
 66 16 Sep 1999  
 67 16 Sep 1999  
 68 16 Mar 1999 9900 0205021  
 69 16 Mar 1999 9903 0010101  
 70 16 Mar 1999 9903 0010101  
 71 (UIMA ) HUMAN GENE 201 1N1  
 72  
 73 human; asthma; asthma; asthma

XX  
 13 WtG 1999 10/15/99/40  
 16 N 15000 AAZ100 2.8  
 XX  
 18 New human vascular endothelial growth factor 2, used for treating, e.g.  
 19 immune disorders and cancers  
 20 Claim 1, Page 1A, 17, 22pp; finalish  
 21  
 22 The present suspension represents vascular endothelial growth factor 2  
 23 (Vegf 2). The VEGF-2 polypeptides have activities similar to VEGF. The  
 24 VEGF-2 polypeptides stimulate the growth of vascular endothelial cells,  
 25 stimulate endothelial cell migration, stimulate angiogenesis, decrease  
 26 blood pressure, and increase blood flow. The polypeptides and  
 27 polypeptides can be used for preventing, treating or ameliorating a  
 28 medical condition. The VEGF-2 polypeptides or polypeptides may be  
 29 used in treating deficiencies or disorders of the immune system, by  
 30 activating or inhibiting the proliferation, differentiation, or  
 31 mobilization (chemotaxis) of immune cells. The edology of these immune  
 32 deficiencies or disorders may be genetic, somatic, such as cancer, or  
 33 some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or  
 34 protein disorders, such as rheumatoid arthritis, common variable  
 35 immunodeficiency, leukocyte syndrome, HIV infection, HIV infection,  
 36 leukocyte adhesion deficiency syndrome, lymphoma, Phagocyte  
 37 leukocyte adhesion deficiency syndrome, severe combined immunodeficiency (SCID),  
 38 Wiskott Aldrich disorder, anemia, thrombocytopoiesis, or hemofilirosis.  
 39 They can also be used to modulate composition or thrombolytic activity  
 40 strongly affecting reactions and conditions such as asthma (airway  
 41 allergic asthma) or other respiratory problems may also be treated.  
 42 Sequence: 419 AA;  
 43  
 44 Query Match 98.98% Score 862 106 119 Length 419  
 45 best local similarity 100.00% Prod. No. 4360 0/2  
 46 Method: 1/2: consensus 0/2 Mismatches 0/2 Indels 0/2 Gaps 0/2  
 47  
 48 2 EELIKFAAHYNTEIK 16  
 49 104 001K1KaaHygn01K 120  
 50  
 51 EELIKFAAHYNTEIK 16  
 52 AAY00510  
 53 AAY00510 standard: Protein: 419 AA  
 54  
 55 AAY00510  
 56 16 Nov 1999 (first entry)  
 57  
 58 Vascular endothelial growth factor 2 (Vegf 2).  
 59  
 60 Human vascular endothelial growth factor 2: VEGF-2  
 61 vascular endothelial cell growth endothelial cell mitogenic  
 62 endothelial cell growth promoting blood flow; immune system  
 63 immune cell; cancer; autoimmune disorder; blood pressure; edema;  
 64 edema; inflammation; common variable immunodeficiency;  
 65 leukocyte adhesion deficiency syndrome; HIV; HIV infection;  
 66 phagocyte; leukocyte; dysfunction; severe combined immunodeficiency;  
 67 Wiskott Aldrich disorder; anemia; thrombocytopoiesis; hemofilirosis;  
 68 allergy; asthma; allergic asthma;  
 69  
 70 human; asthma;  
 71  
 72 W090504 A1  
 73 16 Sep 1999  
 74 16 Sep 1999  
 75 16 Mar 1999 9900 0205021  
 76 16 Mar 1999 9903 0010101  
 77 16 Mar 1999 9903 0010101  
 78 (UIMA ) HUMAN GENE 201 1N1  
 79  
 80 human; asthma; asthma; asthma



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# ALTERNATES

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1 N V 1009 (11EMB001, 12, last sequence update)  
 21 10N 2001 (11EMB001, 17, last annotation update)  
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Index: 1000-192-0000

Genome version 4.5  
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M Protein Protein search using SW model

Run date: February 20, 2002, 16:27:42 : Search time 1.09 seconds  
(without alignment)  
896,455 hits in total of 4405/507

Hit list: 2454  
Postscript scores: 1 MULTIMATCH/AMAVIL.....1141676VH1SRKRLRN 418  
Sequence:

Scoring values: 40-5896.2  
Gapop: 10.0, Gapext: 0.5

Searches: 100093 seqs, 6664847 residues

Total number of hits satisfying chosen parameters: 6004

Minimum for seq length: 0  
Maximum for seq length: 200000000

Postscript scores: Minimum Match: 0.3  
Maximum Match: 1008  
Highest Match: 45 summations

Database: 1: GenBank/99+

Note: This is the number of results predicted by chance to have a score greater than or equal to the score of the best hit (indicated) and is derived by analysis of the total score distribution.

#### Summary

Result	No.	Score	Query Match	Length	ID	Accession
1	1004.5	76.7	419	1	VEHC_HUMAN	U19767 Homo sapien
2	1477.5	74.2	415	1	VEHC_MOUSE	P07658 mus musculu
3	241	10.2	1768	1	VEHC_HUMAN	U19767 Homo sapien
4	199	8.5	216	1	VEHC_MOUSE	U19767 mus musculu
5	191.5	8.1	190	1	VEHC_PIG	U19761 Sus scrofa
6	188.5	8.0	190	1	VEHC_RAT	U19712 Rattus norv
7	179.5	7.6	164	1	VEHC_ZAVPU	P06717 zebra pover
8	179.5	7.6	190	1	VEHC_KOVIN	U19761 Bos taurus
9	174.5	7.4	214	1	VEHC_MOUSE	U19767 mus musculu
10	169	7.2	216	1	VEHC_HUMAN	U19767 Homo sapien
11	164.5	7.0	188	1	VEHC_MOUSE	U19767 mus musculu
12	162.5	6.9	188	1	VEHC_HUMAN	U19767 Homo sapien
13	158.5	6.7	146	1	VEHC_SHIMP	U19767 mus musculu
14	152	6.5	2871	1	VEHC_MOUSE	U19767 mus musculu
15	150	6.4	148	1	VEHC_MOUSE	U19767 mus musculu
16	147.5	6.3	170	1	VEHC_HUMAN	U19767 Homo sapien
17	147	6.2	2871	1	VEHC_PIG	U19761 Sus scrofa
18	146.5	6.2	134	1	VEHC_MOUSE	U19767 mus musculu
19	144	6.1	2871	1	VEHC_HUMAN	U19767 Homo sapien
20	141.5	6.0	3712	1	VEHC_MOUSE	U19767 mus musculu
21	141	6.0	280	1	VEHC_MOUSE	U19767 mus musculu
22	140	5.9	2871	1	VEHC_KOVIN	U19761 Bos taurus
23	138	5.9	337	1	VEHC_HUMAN	U19767 Homo sapien
24	137.5	5.8	1104	1	VEHC_HUMAN	U19767 Homo sapien
25	137.5	5.8	1104	1	VEHC_MOUSE	U19767 mus musculu
26	136.5	5.8	474	1	VEHC_MOUSE	U19767 mus musculu
27	136.5	5.8	1808	1	VEHC_MOUSE	U19767 mus musculu
28	135	5.7	2338	1	VEHC_MOUSE	U19767 mus musculu
29	134.5	5.7	2201	1	VEHC_HUMAN	U19767 Homo sapien
30	134	5.7	2703	1	VEHC_MOUSE	U19767 mus musculu
31	133.5	5.7	810	1	VEHC_HUMAN	U19767 Homo sapien
32	132.5	5.6	810	1	VEHC_HUMAN	U19767 Homo sapien
33	132	5.6	232	1	VEHC_MOUSE	U19767 mus musculu

#### ALIGNMENTS

RESULT	ID	VEHC_HUMAN	STANDARD	PROT	419 AA	
1	VEHC_HUMAN	132	2813	1	VEHC_HUMAN	
2	VEHC_HUMAN	131.5	2541	1	VEHC_MOUSE	
3	VEHC_HUMAN	131	158	1	VEHC_MOUSE	
4	VEHC_HUMAN	129.5	5.5	106	1	VEHC_MOUSE
5	VEHC_HUMAN	129.5	5.5	1408	1	VEHC_MOUSE
6	VEHC_HUMAN	128	5.4	2813	1	VEHC_MOUSE
7	VEHC_HUMAN	128	5.4	4051	1	VEHC_MOUSE
8	VEHC_HUMAN	127	5.4	5376	1	VEHC_MOUSE
9	VEHC_HUMAN	127	5.4	1429	1	VEHC_MOUSE
10	VEHC_HUMAN	126.5	5.4	241	1	VEHC_MOUSE
11	VEHC_HUMAN	126.5	5.4	1807	1	VEHC_MOUSE
12	VEHC_HUMAN	126	5.4	575	1	VEHC_MOUSE
13	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
14	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
15	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
16	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
17	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
18	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
19	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
20	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
21	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
22	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
23	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
24	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
25	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
26	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
27	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
28	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
29	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
30	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
31	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
32	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
33	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
34	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
35	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
36	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
37	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
38	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
39	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
40	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
41	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
42	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
43	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
44	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE
45	VEHC_HUMAN	126	5.4	1807	1	VEHC_MOUSE

































[illegible]

### DECLARATION OF INTEREST

1900; Mott, Acad. Sci. U.S.A. 87, 2628-29 (1990).

Received: November 1, 1997; Accepted: November 1, 1997

$\Delta_{\text{eff}} = \Delta_{\text{eff}}^{\text{eff}} - \Delta_{\text{eff}}^{\text{eff}}$

A. J. P. 1999. *Field Ornithology*, 3rd ed. M. J. 1997. *Nature* 387: 1414-1415. *Avian* 1999.

[illegible]

**Keywords:** *gender inequality; gender discrimination; gender equality; gender equity; gender justice*

[illegible][illegible]

THE UNIVERSITY OF CHICAGO

**THE EFFECT OF VIBRATION ON STABILITY OF A TWO-DOF SYSTEM**

210. O'NEILL, KYLE. What Effect Do Financial Crises Have on the Gender Gap in Pay? *Journal of Applied Social Psychology* 36 (2006): 103-117.

[illegible]
$$148 \text{ g, } \bar{M}_n = 4.5 \times 10^4, \bar{M}_w/\bar{M}_n = 1.38, \text{ } \eta_{\text{inh}} = 0.43 \text{ dl/g, } [\eta] = 0.73 \text{ dl/g, } [\eta]_{\text{calc}} = 0.74 \text{ dl/g}$$
[illegible][illegible][illegible][illegible]

1. *Chrysomelids* (Coleoptera: Chrysomelidae) (1992) 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2

*Received for consideration, February 1, 1990; accepted for publication, February 1, 1991.*

20200909\_24h\_1000\_1000\_1000

A: Local reference quadruplet: A(0.087; M(11); 9006.9038  
A: A(0.087; 10.01); 10.0080

[illegible]

As a consequence of the above, the MSA of the NTPD is considered. The NTPD is defined as the difference between the MSA of the NTPD and the MSA of the NTPD. The NTPD is defined as the difference between the MSA of the NTPD and the MSA of the NTPD.

Ward, D. H., Brophy, J. E., & Smith, T. A. (1989, 1990, 1991, 1992). Vertical and horizontal effects of a new model of the

A. bel. 121000; number: A. 55767; Mulling 901212121.

$$\Delta M = \left\{ \frac{\partial}{\partial t} + \frac{1}{2} \nabla^2 - \frac{1}{2} \nabla \cdot \nabla \right\} \psi$$
[illegible][illegible]

Accepted for publication 10 November 2003  
 Address correspondence to: A. A. Auer, Department of Microbiology, University of Michigan, 400 Tappan Street, Ann Arbor, MI 48106-0602, USA.  
 E-mail: aauer@umich.edu

A. Molodtsov, *1996*: *Practical*  
A. Molodtsov, *1997*: *Practical*

**Keywords:** alcoholism; coping; emotion; family; gender; marital status; personality; social support; stress; women

1. *Chlorophyll a* and *Chlorophyll b* were determined by the method of Lichtenthaler and Whistler (1972). The total chlorophyll content was determined by the method of Arar and Cook (1980). The carotenoid content was determined by the method of Lichtenthaler and Whistler (1972). The total carotenoid content was determined by the method of Arar and Cook (1980). The total protein content was determined by the method of Lowry et al. (1951). The total lipid content was determined by the method of Bligh and Dyer (1959). The total carbohydrate content was determined by the method of Dubois and Gilles (1950). The total nucleic acid content was determined by the method of Burton (1956). The total ash content was determined by the method of AOAC (1990). The total moisture content was determined by the method of AOAC (1990). The total dry matter content was determined by the method of AOAC (1990). The total organic acid content was determined by the method of AOAC (1990). The total alkaloid content was determined by the method of AOAC (1990). The total saponin content was determined by the method of AOAC (1990). The total tannin content was determined by the method of AOAC (1990). The total flavonoid content was determined by the method of AOAC (1990). The total phenolic content was determined by the method of AOAC (1990). The total terpenoid content was determined by the method of AOAC (1990). The total steroid content was determined by the method of AOAC (1990). The total glycoside content was determined by the method of AOAC (1990). The total alkaloid content was determined by the method of AOAC (1990). The total saponin content was determined by the method of AOAC (1990). The total tannin content was determined by the method of AOAC (1990). The total flavonoid content was determined by the method of AOAC (1990). The total phenolic content was determined by the method of AOAC (1990). The total terpenoid content was determined by the method of AOAC (1990). The total steroid content was determined by the method of AOAC (1990). The total glycoside content was determined by the method of AOAC (1990).

1.  $\text{C}_{100}\text{H}_{160}\text{O}_{16}$  (MW = 1444)  $\text{C}_{100}\text{H}_{160}\text{O}_{16}$  (MW = 1444)  $\text{C}_{100}\text{H}_{160}\text{O}_{16}$  (MW = 1444)

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